

#4



PCT09

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/868,123

DATE: 05/15/2002

TIME: 16:09:10

Input Set : A:\EP.txt

Output Set: N:\CRF3\05152002\I868123.raw

ENTERED

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3 <110> APPLICANT: Collins, Mary
4     Donaldson, Debra
5     Fitz, Lora
6     Neben, Tamlyn
7     Whitters, Matthew
8     Wood, Clive
9     Wills-Karp, Marsha
10    Genetics Institute, Inc.
13 <120> TITLE OF INVENTION: Cytokine Receptor Chain
15 <130> FILE REFERENCE: GI 5268A
C--> 17 <140> CURRENT APPLICATION NUMBER: US/09/868,123
C--> 18 <141> CURRENT FILING DATE: 2002-04-02
20 <160> NUMBER OF SEQ ID NOS: 9
22 <170> SOFTWARE: PatentIn Ver. 2.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1525
26 <212> TYPE: DNA
27 <213> ORGANISM: Mus sp.
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (256)..(1404)
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38 aaacagtaga gattcaattt agtgtctaag gtggaaagga ggacaaagag gtcttgatgat 180
40 aactgcctgt gataatacat ttcttgagaa accatattat tgagtagagc tttcagcaca 240
42 ctaaatacctg gagaa atg gct ttt gtg cat atc aga tgc ttg tgt ttc att 291
43     Met Ala Phe Val His Ile Arg Cys Leu Cys Phe Ile
44         1             5             10
46 ctt ctt tgt aca ata act ggc tat tct ttg gag ata aaa gtt aat cct 339
47 Leu Leu Cys Thr Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro
48         15             20             25
50 cct cag gat ttt gaa ata ttg gat cct gga tta ctt ggt tat ctc tat 387
51 Pro Gln Asp Phe Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr
52         30             35             40
54 ttg caa tgg aaa cct cct gtg gtt ata gaa aaa ttt aag ggc tgt aca 435
55 Leu Gln Trp Lys Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr
56 45             50             55             60
58 cta gaa tat gag tta aaa tac cga aat gtt gat agc gac agc tgg aag 483
59 Leu Glu Tyr Glu Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys
60         65             70             75
62 act ata att act agg aat cta att tac aag gat ggg ttt gat ctt aat 531
63 Thr Ile Ile Thr Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn

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64	80	85	90	
66	aaa ggc att gaa gga aag ata cgt acg cat ttg tca gag cat tgt aca	579		
67	Lys Gly Ile Glu Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr			
68	95 100 105			
70	aat gga tca gaa gta caa agt cca tgg ata gaa gct tct tat ggg ata	627		
71	Asn Gly Ser Glu Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile			
72	110 115 120			
74	tca gat gaa gga agt ttg gaa act aaa att cag gac atg aag tgt ata	675		
75	Ser Asp Glu Gly Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile			
76	125 130 135 140			
78	tat tat aac tgg cag tat ttg gtc tgc tct tgg aaa cct ggc aag aca	723		
79	Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Lys Thr			
80	145 150 155			
82	gta tat tct gat acc aac tat acc atg ttt ttc tgg tat gag ggc ttg	771		
83	Val Tyr Ser Asp Thr Asn Tyr Thr Met Phe Phe Trp Tyr Glu Gly Leu			
84	160 165 170			
86	gat cat gcc tta cag tgt gct gat tac ctc cag cat gat gaa aaa aat	819		
87	Asp His Ala Leu Gln Cys Ala Asp Tyr Leu Gln His Asp Glu Lys Asn			
88	175 180 185			
90	gtt gga tgc aaa ctg tcc aac ttg gac tca tca gac tat aaa gat ttt	867		
91	Val Gly Cys Lys Leu Ser Asn Leu Asp Ser Ser Asp Tyr Lys Asp Phe			
92	190 195 200			
94	ttt atc tgt gtt aat gga tct tca aag ttg gaa ccc atc aga tcc agc	915		
95	Phe Ile Cys Val Asn Gly Ser Ser Lys Leu Glu Pro Ile Arg Ser Ser			
96	205 210 215 220			
98	tat aca gtt ttt caa ctt caa aat ata gtt aaa cca ttg cca cca gaa	963		
99	Tyr Thr Val Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Glu			
100	225 230 235			
102	ttc ctt cat att agt gtg gag aat tcc att gat att aga atg aaa tgg	1011		
103	Phe Leu His Ile Ser Val Glu Asn Ser Ile Asp Ile Arg Met Lys Trp			
104	240 245 250			
106	agc aca cct gga gga ccc att cca cca agg tgt tac act tat gaa att	1059		
107	Ser Thr Pro Gly Gly Pro Ile Pro Pro Arg Cys Tyr Thr Tyr Glu Ile			
108	255 260 265			
110	gtg atc cga gaa gac gat att tcc tgg gag tct gcc aca gac aaa aac	1107		
111	Val Ile Arg Glu Asp Asp Ile Ser Trp Glu Ser Ala Thr Asp Lys Asn			
112	270 275 280			
114	gat atg aag ttg aag agg aga gca aat gaa agt gaa gac cta tgc ttt	1155		
115	Asp Met Lys Leu Lys Arg Ala Asn Glu Ser Glu Asp Leu Cys Phe			
116	285 290 295 300			
118	ttt gta aga tgt aag gtc aat ata tat tgt gca gat gat gga att tgg	1203		
119	Phe Val Arg Cys Lys Val Asn Ile Tyr Cys Ala Asp Asp Gly Ile Trp			
120	305 310 315			
122	agc gaa tgg agt gaa gag gaa tgt tgg gaa ggt tac aca ggg cca gac	1251		
123	Ser Glu Trp Ser Glu Glu Glu Cys Trp Glu Gly Tyr Thr Gly Pro Asp			
124	320 325 330			
126	tca aag att att ttc ata gta cca gtt tgt ctt ttc ttt ata ttc ctt	1299		
127	Ser Lys Ile Ile Phe Ile Val Pro Val Cys Leu Phe Phe Ile Phe Leu			
128	335 340 345			

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130 ttg tta ctt ctt tgc ctt att gtg gag aag gaa gaa cct gaa ccc aca 1347
131 Leu Leu Leu Leu Cys Leu Ile Val Glu Lys Glu Glu Pro Glu Pro Thr
132 350 355 360
134 ttg agc ctc cat gtg gat ctg aac aaa gaa gtg tgt gct tat gaa gat 1395
135 Leu Ser Leu His Val Asp Leu Asn Lys Glu Val Cys Ala Tyr Glu Asp
136 365 370 375 380
138 acc ctc tgt taaaccacca atttcttgac atagagccag ccagcaggag 1444
139 Thr Leu Cys
141 tcataattaaa ctcaatttct cttaaaattt cgaatacatc ttcttgaaaa tccaaaaaaa 1504
143 aaaaaaaaaa aaaaactcga g 1525
146 <210> SEQ ID NO: 2
147 <211> LENGTH: 383
148 <212> TYPE: PRT
149 <213> ORGANISM: Mus sp.
151 <400> SEQUENCE: 2
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153 1 5 10 15
155 Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro Pro Gln Asp Phe
156 20 25 30
158 Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr Leu Gln Trp Lys
159 35 40 45
161 Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr Leu Glu Tyr Glu
162 50 55 60
164 Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys Thr Ile Ile Thr
165 65 70 75 80
167 Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu
168 85 90 95
170 Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr Asn Gly Ser Glu
171 100 105 110
173 Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile Ser Asp Glu Gly
174 115 120 125
176 Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile Tyr Tyr Asn Trp
177 130 135 140
179 Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Lys Thr Val Tyr Ser Asp
180 145 150 155 160
182 Thr Asn Tyr Thr Met Phe Phe Trp Tyr Glu Gly Leu Asp His Ala Leu
183 165 170 175
185 Gln Cys Ala Asp Tyr Leu Gln His Asp Glu Lys Asn Val Gly Cys Lys
186 180 185 190
188 Leu Ser Asn Leu Asp Ser Ser Asp Tyr Lys Asp Phe Phe Ile Cys Val
189 195 200 205
191 Asn Gly Ser Ser Lys Leu Glu Pro Ile Arg Ser Ser Tyr Thr Val Phe
192 210 215 220
194 Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Glu Phe Leu His Ile
195 225 230 235 240
197 Ser Val Glu Asn Ser Ile Asp Ile Arg Met Lys Trp Ser Thr Pro Gly
198 245 250 255
200 Gly Pro Ile Pro Pro Arg Cys Tyr Thr Tyr Glu Ile Val Ile Arg Glu
201 260 265 270

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Input Set : A:\EP.txt

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203 Asp Asp Ile Ser Trp Glu Ser Ala Thr Asp Lys Asn Asp Met Lys Leu
204      275      280      285
206 Lys Arg Arg Ala Asn Glu Ser Glu Asp Leu Cys Phe Phe Val Arg Cys
207      290      295      300
209 Lys Val Asn Ile Tyr Cys Ala Asp Asp Gly Ile Trp Ser Glu Trp Ser
210 305      310      315      320
212 Glu Glu Glu Cys Trp Glu Gly Tyr Thr Gly Pro Asp Ser Lys Ile Ile
213      325      330      335
215 Phe Ile Val Pro Val Cys Leu Phe Phe Ile Phe Leu Leu Leu Leu Leu
216      340      345      350
218 Cys Leu Ile Val Glu Lys Glu Glu Pro Glu Pro Thr Leu Ser Leu His
219      355      360      365
221 Val Asp Leu Asn Lys Glu Val Cys Ala Tyr Glu Asp Thr Leu Cys
222      370      375      380
225 <210> SEQ ID NO: 3
226 <211> LENGTH: 1369
227 <212> TYPE: DNA
228 <213> ORGANISM: Homo sapiens
230 <220> FEATURE:
231 <221> NAME/KEY: CDS
232 <222> LOCATION: (103)..(1245)
234 <400> SEQUENCE: 3
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237 ggcgggggaga gaggcaatat caaggtttta aatctcggag aa atg gct ttc gtt 114
238      Met Ala Phe Val
239      1
241 tgc ttg gct atc gga tgc tta tat acc ttt ctg ata agc aca aca ttt 162
242 Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile Ser Thr Thr Phe
243 5      10      15      20
245 ggc tgt act tca tct tca gac acc gag ata aaa gtt aac cct cct cag 210
246 Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val Asn Pro Pro Gln
247      25      30      35
249 gat ttt gag ata gtg gat ccc gga tac tta ggt tat ctc tat ttg caa 258
250 Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln
251      40      45      50
253 tgg caa ccc cca ctg tct ctg gat cat ttt aag gaa tgc aca gtg gaa 306
254 Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val Glu
255      55      60      65
257 tat gaa cta aaa tac cga aac att ggt agt gaa aca tgg aag acc atc 354
258 Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile
259      70      75      80
261 att act aag aat cta cat tac aaa gat ggg ttt gat ctt aac aag ggc 402
262 Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly
263 85      90      95      100
265 att gaa gcg aag ata cac acg ctt tta cca tgg caa tgc aca aat gga 450
266 Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly
267      105      110      115
269 tca gaa gtt caa agt tcc tgg gca gaa act act tat tgg ata tca cca 498
270 Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro

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Input Set : A:\EP.txt

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271		120		125		130		
273	caa gga att cca gaa act aaa gtt cag gat atg gat tgc gta tat tac							546
274	Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp Cys Val Tyr Tyr							.
275		135		140		145		
277	aat tgg caa tat tta ctc tgt tct tgg aaa cct ggc ata ggt gta ctt							594
278	Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly Ile Gly Val Leu							
279		150		155		160		
281	ctt gat acc aat tac aac ttg ttt tac tgg tat gag ggc ttg gat cat							642
282	Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His							
283	165		170		175		180	
285	gca tta cag tgt gtt gat tac atc aag gct gat gga caa aat ata gga							690
286	Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly Gln Asn Ile Gly							
287		185		190		195		
289	tgc aga ttt ccc tat ttg gag gca tca gac tat aaa gat ttc tat att							738
290	Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys Asp Phe Tyr Ile							
291		200		205		210		
293	tgt gtt aat gga tca tca gag aac aag cct atc aga tcc agt tat ttc							786
294	Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg Ser Ser Tyr Phe							
295		215		220		225		
297	act ttt cag ctt caa aat ata gtt aaa cct ttg ccg cca gtc tat ctt							834
298	Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Val Tyr Leu							
299		230		235		240		
301	act ttt act cgg gag agt tca tgt gaa att aag ctg aaa tgg agc ata							882
302	Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu Lys Trp Ser Ile							
303	245		250		255		260	
305	cct ttg gga cct att cca gca agg tgt ttt gat tat gaa att gag atc							930
306	Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr Glu Ile Glu Ile							
307		265		270		275		
309	aga gaa gat gat act acc ttg gtg act gct aca gtt gaa aat gaa aca							978
310	Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val Glu Asn Glu Thr							
311		280		285		290		
313	tac acc ttg aaa aca aca aat gaa acc cga caa tta tgc ttt gta gta							1026
314	Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu Cys Phe Val Val							
315		295		300		305		
317	aga agc aaa gtg aat att tat tgc tca gat gac gga att tgg agt gag							1074
318	Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu							
319		310		315		320		
321	tgg agt gat aaa caa tgc tgg gaa ggt gaa gac cta tcg aag aaa act							1122
322	Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu Ser Lys Lys Thr							
323	325		330		335		340	
325	ttg cta cgt ttc tgg cta cca ttt ggt ttc atc tta ata tta gtt ata							1170
326	Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu Ile Leu Val Ile							
327		345		350		355		
329	ttt gta acc ggt ctg ctt ttg cgt aag cca aac acc tac cca aaa atg							1218
330	Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr Tyr Pro Lys Met							
331		360		365		370		
333	att cca gaa ttt ttc tgt gat aca tga agactttcca tatcaagaga							1265
334	Ile Pro Glu Phe Phe Cys Asp Thr							
335		375		380				

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/868,123

DATE: 05/15/2002

TIME: 16:09:12

Input Set : A:\EP.txt

Output Set: N:\CRF3\05152002\I868123.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application Number

L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date